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RAW SEQUENCE LISTING

DATE: 04/26/2002

PATENT APPLICATION: US/09/902,772

TIME: 14:00:29

Input Set : N:\Crf3\RULE60\09902772.raw

Output Set: N:\CRF3\04262002\I902772.raw

1 <110> APPLICANT: Chugai Seiyaku Kabushiki Kaisha, 5001, Iwamoto et
 2 <120> TITLE OF INVENTION: Cell Calcification Suppressing Proteins and Genes of
 3 the Proteins
 4 <130> FILE REFERENCE: chugai seiyaku kabushiki kaisha 5001
 5 <140> CURRENT APPLICATION NUMBER: 09/902,772
 6 <141> CURRENT FILING DATE: 2001-07-12
 8 <150> PRIOR APPLICATION NUMBER: US/08/878,177
 9 <151> PRIOR FILING DATE: 1997-06-18
 12 <160> NUMBER OF SEQ ID NOS: 7
 13 <170> SOFTWARE: PatentIn Ver. 2.0
 15 <210> SEQ ID NO: 1
 16 <211> LENGTH: 1447
 17 <212> TYPE: DNA
 18 <213> ORGANISM: C-11 gene, c-erg gene w/ deletion, chicken DNA
 19 <400> SEQUENCE: 1
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 21 ttatggcaag cactattaag gaagcattat cagtgggtgag tgaagaccag tccttggttg 120
 22 agtgtgccta cggatcgccc caccttgcaa agacagaaat gacagcctcc tcttcagtg 180
 23 aatatgggca aacatcaaag atgagccgc gcgttcccca gcaggactgg ttatcacagc 240
 24 ccccgccag agttaccatt aagatggagt gtaacccaaa ccaggttaat gggtaagga 300
 25 attcaoctga tgactgcagc gtggcaaaaag gagggaaaat ggtagcagt tcagacaatg 360
 26 ttgggatgaa ctatggaagc tacatggaag agaagcatat tccgcctcca aatatgacaa 420
 27 ccaatgaacg aagagttatt gtgccagcag atcctacgtt atggagcaca gaccatgtac 480
 28 ggcagtggct ggagtgggca gtgaaggagt atggtcttcc agacgtggac atcttggttg 540
 29 tccagaacat tgatgggaaa gagttgtgta aaatgaccaa agatgacttc cagagactca 600
 30 cgccgagcta taacgcagat atcctcctgt cacacctaca ctacctcaga gagagaggag 660
 31 ccacttttat ttttccaaat acatcagttt acccagaagc aacgcaaaga ataacaacaa 720
 32 ggccagattt accttatgag caagcgagga gatcagcgtg gacgagtcac agccatccca 780
 33 ctcagtcaaa agctacccaa ccacatctt caacagtgcc caaaacagaa gaccagcgtc 840
 34 ctcagttaga tcttatcag attcttgga cgaaccagcag ccgtcttgca aatccaggga 900
 35 gtgggcagat acagctatgg cagttcctac tggagcttct gtcggacagc tccaactcca 960
 36 actgcatcac ctgggagggc acaaatgggg agttcaagat gacagaccct gatgaagtgg 1020
 37 ctcggcgttg gggagagagg aaaagcaaac ctaacatgaa ctatgacaaa ctacgccgtg 1080
 38 cacttcgcta ctactatgac aaaaatatta tgactaaagt tcatggtaaa cgctatgcct 1140
 39 acaaatgtga tttccacgga atcgctcagg cctccagcc tcacctcca gaatcatcca 1200
 40 tgtacaaata cccatcagac ctcccctaca tgagttccta ccatgcacac cccagaaga 1260
 41 tgaactttgt agctcccat cccctgctt tgcccgtaac ctcatccagc tttttgtctg 1320
 42 cccctaatac atactggaat tcaccaactg gaggcatac cccaatacc aggtgccag 1380
 43 ctgctcatat gccttcccat cttggcacct actactaagt ggggaaagaa agaaagcgcc 1440
 44 aagaaaaa 1447
 46 <210> SEQ ID NO: 2
 47 <211> LENGTH: 451
 48 <212> TYPE: PRT

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49 <213> ORGANISM: protein sequence from C-11 gene

50 <400> SEQUENCE: 2

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51 Met Ala Ser Thr Ile Lys Glu Ala Leu Ser Val Val Ser Glu Asp Gln
52 1 5 10 15
53 Ser Leu Phe Glu Cys Ala Tyr Gly Ser Pro His Leu Ala Lys Thr Glu
54 20 25 30
55 Met Thr Ala Ser Ser Ser Ser Glu Tyr Gly Gln Thr Ser Lys Met Ser
56 35 40 45
57 Pro Arg Val Pro Gln Gln Asp Trp Leu Ser Gln Pro Pro Ala Arg Val
58 50 55 60
59 Thr Ile Lys Met Glu Cys Asn Pro Asn Gln Val Asn Gly Ser Arg Asn
60 65 70 75 80
61 Ser Pro Asp Asp Cys Ser Val Ala Lys Gly Gly Lys Met Val Ser Ser
62 85 90 95
63 Ser Asp Asn Val Gly Met Asn Tyr Gly Ser Tyr Met Glu Glu Lys His
64 100 105 110
65 Ile Pro Pro Pro Asn Met Thr Thr Asn Glu Arg Arg Val Ile Val Pro
66 115 120 125
67 Ala Asp Pro Thr Leu Trp Ser Thr Asp His Val Arg Gln Trp Leu Glu
68 130 135 140
69 Trp Ala Val Lys Glu Tyr Gly Leu Pro Asp Val Asp Ile Leu Leu Phe
70 145 150 155 160
71 Gln Asn Ile Asp Gly Lys Glu Leu Cys Lys Met Thr Lys Asp Asp Phe
72 165 170 175
73 Gln Arg Leu Thr Pro Ser Tyr Asn Ala Asp Ile Leu Leu Ser His Leu
74 180 185 190
75 His Tyr Leu Arg Glu Arg Gly Ala Thr Phe Ile Phe Pro Asn Thr Ser
76 195 200 205
77 Val Tyr Pro Glu Ala Thr Gln Arg Ile Thr Thr Arg Pro Asp Leu Pro
78 210 215 220
79 Tyr Glu Gln Ala Arg Arg Ser Ala Trp Thr Ser His Ser His Pro Thr
80 225 230 235 240
81 Gln Ser Lys Ala Thr Gln Pro Ser Ser Ser Thr Val Pro Lys Thr Glu
82 245 250 255
83 Asp Gln Arg Pro Gln Leu Asp Pro Tyr Gln Ile Leu Gly Pro Thr Ser
84 260 265 270
85 Ser Arg Leu Ala Asn Pro Gly Ser Gly Gln Ile Gln Leu Trp Gln Phe
86 275 280 285
87 Leu Leu Glu Leu Leu Ser Asp Ser Ser Asn Ser Asn Cys Ile Thr Trp
88 290 295 300
89 Glu Gly Thr Asn Gly Glu Phe Lys Met Thr Asp Pro Asp Glu Val Ala
90 305 310 315 320
91 Arg Arg Trp Gly Glu Arg Lys Ser Lys Pro Asn Met Asn Tyr Asp Lys
92 325 330 335
93 Leu Ser Arg Ala Leu Arg Tyr Tyr Tyr Asp Lys Asn Ile Met Thr Lys
94 340 345 350
95 Val His Gly Lys Arg Tyr Ala Tyr Lys Phe Asp Phe His Gly Ile Ala
96 355 360 365
97 Gln Ala Leu Gln Pro His Pro Pro Glu Ser Ser Met Tyr Lys Tyr Pro

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98          370          375          380
99      Ser Asp Leu Pro Tyr Met Ser Ser Tyr His Ala His Pro Gln Lys Met
100      385          390          395          400
101      Asn Phe Val Ala Pro His Pro Pro Ala Leu Pro Val Thr Ser Ser Ser
102          405          410          415
103      Phe Phe Ala Ala Pro Asn Pro Tyr Trp Asn Ser Pro Thr Gly Gly Ile
104          420          425          430
105      Tyr Pro Asn Thr Arg Leu Pro Ala Ala His Met Pro Ser His Leu Gly
106          435          440          445
107      Thr Tyr Tyr
108          450
110 <210> SEQ ID NO: 3
111 <211> LENGTH: 1528
112 <212> TYPE: DNA
113 <213> ORGANISM: c-erg gene, chicken DNA
114 <400> SEQUENCE: 3
115      gaattccgcg aacgaataat tattattagc aattattagc gatcaataat cttgatcaca 60
116      ttatggcaag cactattaag gaagcattat cagtgggtgag tgaagaccag tccttggttg 120
117      agtgtgccta cggatcgccc caccttgcaa agacagaaat gacagcctcc tcttcagtg 180
118      aatatgggca aacatcaaag atgagccgcg gcgttcccca gcaggactgg ttatcacagc 240
119      ccccggccag agttaccatt aagatggagt gtaacccaaa ccaggttaat gggtaagga 300
120      attcacctga tgactgcagc gtggcaaaaag gagggaaaat ggtagcagt tcagacaatg 360
121      ttgggatgaa ctatggaagc tacatggaag agaagcatat tccgcctcca aatatgacaa 420
122      ccaatgaacg aagagttatt gtgccagcag atcctacgtt atggagcaca gaccatgtac 480
123      ggcagtggct ggagtgggca gtgaaggagt atggtcttcc agacgtggac atcttggtgt 540
124      tccagaacat tgatgggaaa gagttgtgta aaatgaccaa agatgacttc cagagactca 600
125      cgccgagcta taacgcagat atcctcctgt cacacctaca ctacctcaga gagactcctc 660
126      ttccacattt gacttcagat gatgttgata aggccttaca aaactctcca cggttaatgc 720
127      atgctagaaa cacaggagga gccactttta tttttccaaa tacatcagtt taccagaag 780
128      caacgcaaag aataacaaca aggccagatt taccttatga gcaagcgagg agatcagcgt 840
129      ggacgagtca cagccatccc actcagtcga aagctaccca accatcatct tcaacagtgc 900
130      ccaaaacaga agaccagcgt cctcagttag atccttatca gattcttgga ccgaccagca 960
131      gccgtcttgc aaatccaggg agtgggcaga tacagctatg gcagttccta ctggagcttc 1020
132      gtgcggacag ctccaactcc aactgcata cctgggaggg caaaaatggg gagttcaaga 1080
133      tgacagaccc tgatgaagtg gctcggcggt ggggagagag gaaaagcaaa cctaactga 1140
134      actatgacaa actcagccgt gcacttcgct actactatga caaaaatatt atgactaaag 1200
135      ttcatggtaa acgctatgcc tacaaatttg atttccacgg aatcgctcag gccctccagc 1260
136      ctcaccctcc agaatcatcc atgtacaaat acccatcaga cctcccctac atgagttcct 1320
137      accatgcaca cccccagaag atgaactttg tagctcccca tccccctgct ttgcccgtaa 1380
138      cctcatccag cttttttgct gccctaatc catactggaa ttcaccaact ggaggcatct 1440
139      accccaatac caggctgcca gctgctcata tgccttccca tcttggcacc tactactaag 1500
140      tggggaaaaga aagaaagcgc caagaaaa 1528
142 <210> SEQ ID NO: 4
143 <211> LENGTH: 478
144 <212> TYPE: PRT
145 <213> ORGANISM: protein sequence from c-erg gene
146 <400> SEQUENCE: 4
147      Met Ala Ser Thr Ile Lys Glu Ala Leu Ser Val Val Ser Glu Asp Gln
148          1          5          10          15

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149 Ser Leu Phe Glu Cys Ala Tyr Gly Ser Pro His Leu Ala Lys Thr Glu
150           20           25           30
151 Met Thr Ala Ser Ser Ser Ser Glu Tyr Gly Gln Thr Ser Lys Met Ser
152           35           40           45
153 Pro Arg Val Pro Gln Gln Asp Trp Leu Ser Gln Pro Pro Ala Arg Val
154           50           55           60
155 Thr Ile Lys Met Glu Cys Asn Pro Asn Gln Val Asn Gly Ser Arg Asn
156           65           70           75           80
157 Ser Pro Asp Asp Cys Ser Val Ala Lys Gly Gly Lys Met Val Ser Ser
158           85           90           95
159 Ser Asp Asn Val Gly Met Asn Tyr Gly Ser Tyr Met Glu Glu Lys His
160           100          105          110
161 Ile Pro Pro Pro Asn Met Thr Thr Asn Glu Arg Arg Val Ile Val Pro
162           115          120          125
163 Ala Asp Pro Thr Leu Trp Ser Thr Asp His Val Arg Gln Trp Leu Glu
164           130          135          140
165 Trp Ala Val Lys Glu Tyr Gly Leu Pro Asp Val Asp Ile Leu Leu Phe
166           145          150          155          160
167 Gln Asn Ile Asp Gly Lys Glu Leu Cys Lys Met Thr Lys Asp Asp Phe
168           165          170          175
169 Gln Arg Leu Thr Pro Ser Tyr Asn Ala Asp Ile Leu Leu Ser His Leu
170           180          185          190
171 His Tyr Leu Arg Glu Thr Pro Leu Pro His Leu Thr Ser Asp Asp Val
172           195          200          205
173 Asp Lys Ala Leu Gln Asn Ser Pro Arg Leu Met His Ala Arg Asn Thr
174           210          215          220
175 Gly Gly Ala Thr Phe Ile Phe Pro Asn Thr Ser Val Tyr Pro Glu Ala
176           225          230          235          240
177 Thr Gln Arg Ile Thr Thr Arg Pro Asp Leu Pro Tyr Glu Gln Ala Arg
178           245          250          255
179 Arg Ser Ala Trp Thr Ser His Ser His Pro Thr Gln Ser Lys Ala Thr
180           260          265          270
181 Gln Pro Ser Ser Ser Thr Val Pro Lys Thr Glu Asp Gln Arg Pro Gln
182           275          280          285
183 Leu Asp Pro Tyr Gln Ile Leu Gly Pro Thr Ser Ser Arg Leu Ala Asn
184           290          295          300
185 Pro Gly Ser Gly Gln Ile Gln Leu Trp Gln Phe Leu Leu Glu Leu Leu
186           305          310          315          320
187 Ser Asp Ser Ser Asn Ser Asn Cys Ile Thr Trp Glu Gly Thr Asn Gly
188           325          330          335
189 Glu Phe Lys Met Thr Asp Pro Asp Glu Val Ala Arg Arg Trp Gly Glu
190           340          345          350
191 Arg Lys Ser Lys Pro Asn Met Asn Tyr Asp Lys Leu Ser Arg Ala Leu
192           355          360          365
193 Arg Tyr Tyr Tyr Asp Lys Asn Ile Met Thr Lys Val His Pro Pro Glu
194           370          375          380
195 Ser Ser Met Tyr Lys Tyr Pro Ser Asp Leu Pro Tyr Met Ser Ser Tyr
196           385          390          395          400
197 His Gly Lys Arg Tyr Ala Tyr Lys Phe Asp Phe His Gly Ile Ala Gln

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```

198                               405                               410                               415
199      Ala Leu Gln Pro His Ala His Pro Gln Lys Met Asn Phe Val Ala Pro
200                               420                               425                               430
201      His Pro Pro Ala Leu Pro Val Thr Ser Ser Ser Phe Phe Ala Ala Pro
202                               435                               440                               445
203      Asn Pro Tyr Trp Asn Ser Pro Thr Gly Gly Ile Tyr Pro Asn Thr Arg
204                               450                               455                               460
205      Leu Pro Ala Ala His Met Pro Ser His Leu Gly Thr Tyr Tyr
206      465                               470                               475

208 <210> SEQ ID NO: 5
209 <211> LENGTH: 23
210 <212> TYPE: DNA
211 <213> ORGANISM: primer for isolation of C-11 and c-erg genes
212 <400> SEQUENCE: 5
213      atcttgatca cattatggca agc                                     23
215 <210> SEQ ID NO: 6
216 <211> LENGTH: 25
217 <212> TYPE: DNA
218 <213> ORGANISM: primer for isolation of C-11 and c-erg genes
219 <400> SEQUENCE: 6
220      cacattatgg caagcactat taagg                                     25
222 <210> SEQ ID NO: 7
223 <211> LENGTH: 25
224 <212> TYPE: DNA
225 <213> ORGANISM: primer for isolation of C-11 and c-erg genes
226 <400> SEQUENCE: 7
227      cacttagtag taggtgccaa gatgg                                     25

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VERIFICATION SUMMARY

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